

INFORMAL SEQUENCE LISTING

NOVEL PROTEINS

SEQ ID NO:1

(cDNA Sequence of PN7740)

CGAGAATTTCCAGCAGGCAAGGCAGTGGCCGCTTTGACTGCTTGCTTCGGAGATCCGAG
ACGACGGAGAAGGCACTCTTATTTACCGACCAAGAAAGCTCCTCCCCCGTCCTCCGTTA
GCTAATTAAAACATTTTTTCAGGGACGTAGCCATCCAGAGACATTCCATTATTGTTCCAT
TGACCTTTCCCTCATCACTGAGTCCTTTGGAGCTGAGTTATGTCAACAGCTGCCTTAAT
TACTTTGGTCAGAAGTGGTGGGAACCAGGTGAGAAGGAGAGTGCTGCTAAGCTCCCGCC
TGCTGCAGGACGACAGGCGGGTGACACCCACGTGCCACAGCTCCACTTCAGAGCCTAGG
TGTTCTCGGTTTGACCCAGATGGTAGTGGGAGTCCAGCTACCTGGGACAATTTTGGGAT
CTGGGATAACCGCATTGATGAGCCAATTCTGCTGCCACCCAGCATTAAGTATGGCAAGC
CAATTCCCAAATCAGCTTGAAAAATGTGGGGTGCGCCTCACAGATTGGCAAACGGAAA
GAGAATGAAGATCGGTTTGACTTCGCTCAGCTGACAGATGAGGTCCTGTACTTTGCAGT
GTATGATGGACACGGTGGACCTGCAGCAGCTGATTTCTGTCATACCCACATGGAGAAAT
GTATTATGGATTTGCTTCCTAAGGAGAAGAACTTGAAACTCTGTTGACCTTGGCTTTT
CTAGAAATAGATAAAGCCTTTTTCGAGTCATGCCCGCCTGTCTGCTGATGCAACTCTTCT
GACCTCTGGGACTACTGCAACAGTAGCCCTATTGCGAGATGGTATTGAACTGGTTGTAG
CCAGTGTTGGGGACAGCCGGGCTATTTTGTGTAGAAAAGGAAAACCCATGAAGCTGACC
ATTGACCATACTCCAGAAAGAAAAGATGAAAAAGAAAGGATCAAGAAATGTGGTGGTTT
TGTAGCTTGGAATAGTTTGGGGCAGCCTCACGTAAATGGCAGGCTTGCAATGACAAGAA
GTATTGGAGATTTGGACCTTAAGACCAGTGGTGTATAGCAGAACCTGAAACTAAGAGG
ATTAAGTTACATCATGCTGATGACAGCTTCCTGGTCTCTACCAACAGATGGAATTAAGT
CATGGTGAATAGTCAAGAGATTTGTGACTTTGTCAATCAGTGCCATGATCCCAACGAAG
CAGCCCATGCGGTGACTGAACAGGCAATACAGTACGGTACTGAGGATAACAGTACTGCA
GTAGTAGTGCCCTTTTGGTGCCTGGGGAAAATATAAGAACTCTGAAATCAACTTCTCATT
CAGCAGAAGCTTTGCCTCCAGTGGACGATGGGCCTGATTACCAGCTGGGACTTAGAGTT
TCTGTGCAACAGTTTTTCACTGAGCATGTCAAGAAACTGATAAGATCAAAAAGGTCTCC
TAACTCACTAGATCAGCGCACAAGTCAGTGTAAACCACTTAGATAGTAGTTTTTTTCATA
AATGCTCATCATATTTATGTTCCGCTGTACATGTTTCAATATAAATATATGTGTAGTGAA
GCTACTGTGAGTCTTTAAATGGAAAGAGCAAATGAGAAGTGGTTTGGATACACTTGATG
AGAGATGAGAGTGTCACATTAATAATTTTTTAAGACTCTTAGGCAGCTATGGGTTTCTTT
TGATCATTTTTTGTCTTTTATTCATTTGAACACGTTTTTGAAGTTCTTCAAACTAGTCA
GTTTGAATTTTGAACAGCTATTCAATATGTGATCTCCAAGTTTAAAAAATTTTTTTCCA
GACTTCCCTAATCCTAAAATGCGAGTTTTTATTTTTTAATAACTGTACCAAGGAATAAGT
ATGAAAACAGTTCTCTGTTACCATATTTTGTATTCTGGACCACTTACTGGTGAAAGCAA
CCATGCAAAAGAAATTAATTTGGCCAGGCACAGTGGCTCATGCCTGTAATCCCAAATTG
CTGGGATTACAGCACTGTGCCCTCCTAGGAAATTATTTTTTAAGTGAATTTTATTTTTT
ATTTTTTTTAGGATTTTGGTAGAGAATGAGTAGGCCTACTCATCAATATCAAACAGGAC
ATTTAGTTTCTTTCCTTAGAACAGACATAAATTTAATTTTCATGGTAATATGATAATAAG
AAAATGCTTCTATTTTTCTTTAGCACCTCCATGGTTCTCATATACCCATGTCTGTAAAA
AGTGACATGAGAATTTTGTGGGTTACATTTTATTGTATTTATTAGATTGCTTATATA
GATGACTTAGGCAGAAATAAAGTCATGTCTTTAGAAGGTGAACAAGCCAAGTTGTGATG

GCCTGCCTTTTGGCTTTTGGCAGTTGGGATGAGAACAATTGACTCTCCCATTTGGTTGTTA
GATAGTTGAAATGGTGCCTTGGTGGTCATACTTAGTGTTCTAGGCTGTGAAATCATGGA
GTTCTTCCACTTCCAAGAATGACTCATTGCTGTTGGATTCTAGTACAGAATTTAGCAG
CCTGATGTGTCCCCAACTGATTTAATTTCTACTGAAGTGCCCTTGTGTACATTTGTTT
TGTAATTTACCAAAGTACTACCTGAGTGTATAATGACTCCTGCAGTGAGTTAATGTAAT
TGCTGCTTTGACCATTGTTTTAAATCTGTGTACTAGAGTAACTGTGAGCAGAATGAAAT
CACATTATCTCAGTGTTCAAAATATCATTCTAATAAAGTACATGCATTAAACAATTTTA
AAAAAACAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:2
(Amino Acid Sequence of PN7740)

MSTAALITLVRSGGNQVRRRVLLSSRLLQDDRRVTPPTCHSSTSEPRCSRFPDPSGSPA
TWDNFGIWDNRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFDFAQLTD
EVLYFAVYDGHGGPAAADFCHTHMEKCIDLLPKEKNLETLLTLAFLEIDKAFSSHARL
SADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKLTIDHTPERKDEKER
IKKCGGFVAWNSLGQPHVNGRLAMTRSIGDLDLKTSGVIAEPETKRIKLHHADDSFLVL
TTDGINFMVNSQEICDFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
SEINFSFSRSFASSGRWA

Antisense Oligonucleotides Directed Against:

BAT3

SEQ ID NO:3 5' -ttaggctccatggccgacag-3'
SEQ ID NO:4 5' -aggctccatggccgacaggt-3'
SEQ ID NO:5 5' -gctccatggccgacaggtct-3'

GLYP

SEQ ID NO:6 5' -cggagctccatggcggggcc-3'
SEQ ID NO:7 5' -gagctccatggcggggccgg-3'
SEQ ID NO:8 5' -gctccatggcggggccggcg-3'

LRP2

SEQ ID NO:9 5' -ccgcgatccatctccgcgac-3'
SEQ ID NO:10 5' -gcgatccatctccgcgacgg-3'
SEQ ID NO:11 5' -gatccatctccgcgacggtc-3'

LRPAP1

SEQ ID NO:12 5'-cgcgggcgccatcatcccccg-3'
SEQ ID NO:13 5'-cggcgccatcatcccccgct-3'
SEQ ID NO:14 5'-gcgccatcatcccccgctca-3'

TTR

SEQ ID NO:15 5'-tgagaagccatcctgccaag-3'
SEQ ID NO:16 5'-agaagccatcctgccaagaa-3'
SEQ ID NO:17 5'-aagccatcctgccaagaatg-3'

APBB1 (710)

SEQ ID NO:18 5'-ggaacagacatggccttggc-3'
SEQ ID NO:19 5'-aacagacatggccttggcag-3'
SEQ ID NO:20 5'-cagacatggccttggcagct-3'

PN7740

SEQ ID NO:21 5'-gctgttgacataactcagct-3'
SEQ ID NO:22 5'-tgttgacataactcagctcc-3'
SEQ ID NO:23 5'-ttgacataactcagctccaa-3'

APBA1

SEQ ID NO:24 5'-aagtggttcatggtgggagtg-3'
SEQ ID NO:25 5'-gtggttcatggtgggagtcg-3'
SEQ ID NO:26 5'-ggttcatggtgggagtcgga-3'

GLUL

SEQ ID NO:27 5'-gaggtggtcatggtggaagg-3'
SEQ ID NO:28 5'-ggtggtcatggtggaagg-3'
SEQ ID NO:29 5'-tggtcatggtggaagg-3'

KIAA0427

SEQ ID NO:30 5'-gagttttccatccctccagc-3'
SEQ ID NO:31 5'-gttttccatccctccagctc-3'
SEQ ID NO:32 5'-tttccatccctccagctcag-3'

PS1(467)

SEQ ID NO:33 5'-aactctgtcattggagcaac-3'
SEQ ID NO:34 5'-ctctgtcattggagcaactg-3'
SEQ ID NO:35 5'-ctgtcattggagcaactgta-3'

CASK

SEQ ID NO:36 5'-tcgtcggccatggtccggag-3'
SEQ ID NO:37 5'-gtcggccatggtccggaggg-3'
SEQ ID NO:38 5'-cggccatggtccggagggga-3'

DMD(3685)

SEQ ID NO:39 5'-caccaaagcattttgaaaag-3'
SEQ ID NO:40 5'-ccaaagcattttgaaaagt-3'
SEQ ID NO:41 5'-aaagcattttgaaaagtga-3'

CIB

SEQ ID NO:42 5'-gagccccccatcgccccgcc-3'

SEQ ID NO:43 5'-gccccccatcgccccgccgc-3'

SEQ ID NO:44 5'-cccccatcgccccgccgcgc-3'

S1P

SEQ ID NO:45 5'-acaagcttcatggtcacaag-3'

SEQ ID NO:46 5'-aagcttcatggtcacaagcg-3'

SEQ ID NO:47 5'-gcttcatggtcacaagcgaa-3'

APBA2

SEQ ID NO:48 5'-cggtgggccatggcagtcgt-3'

SEQ ID NO:49 5'-gtgggcatggcagtcgttc-3'

SEQ ID NO:50 5'-gggcatggcagtcgttcac-3'

PGAD

SEQ ID NO:51 5'-gcaaaagccattgctggagt-3'

SEQ ID NO:52 5'-aaaagccattgctggagttg-3'

SEQ ID NO:53 5'-aagccattgctggagttggc-3'

ETFB

SEQ ID NO:54 5'-agctccgccatcttcccgcc-3'

SEQ ID NO:55 5'-ctccgccatcttcccgccgc-3'

SEQ ID NO:56 5'-ccgccatcttcccgccgcag-3'

GAPD

SEQ ID NO:57 5'-accttccccatggtgtctga-3'

SEQ ID NO:58 5'-cttccccatggtgtctgagc-3'

SEQ ID NO:59 5'-tccccatggtgtctgagcga-3'

PS2 (448)

SEQ ID NO:60 5'-aatgtgagcatagccctgcc-3'

SEQ ID NO:61 5'-tgtgagcatagccctgcctc-3'

SEQ ID NO:62 5'-tgagcatagccctgcctctg-3'

ATPMB

SEQ ID NO:63 5'-aatgaagtcatttttaaccc-3'

SEQ ID NO:64 5'-tgaagtcatttttaaccctt-3'

SEQ ID NO:65 5'-aagtcatttttaacccttat-3'

GASP

SEQ ID NO:66 5'-gccccagtcatggtacaagt-3'

SEQ ID NO:67 5'-cccagtcatggtacaagtta-3'

SEQ ID NO:68 5'-cagtcatggtacaagttaca-3'

PI4K

SEQ ID NO:69 5'-atctcccgcataactacag-3'

SEQ ID NO:70 5'-ctcccgcataactacaggt-3'

SEQ ID NO:71 5'-cccgcataactacaggtac-3'

5HT-2A

SEQ ID NO:72 5'-agaatatccatgtctaagcc-3'
SEQ ID NO:73 5'-aatatccatgtctaagccag-3'
SEQ ID NO:74 5'-tatccatgtctaagccagaa-3'

KIAA0351

SEQ ID NO:75 5'-ctcttgtagatagctctccag-3'
SEQ ID NO:76 5'-cttgtagatagctctccaggc-3'
SEQ ID NO:77 5'-tgtacatagctctccaggcca-3'

TRIO(2861)

SEQ ID NO:78 5'-atagctttcatttcacggtt-3'
SEQ ID NO:79 5'-agctttcatttcacgtttt-3'
SEQ ID NO:80 5'-ctttcatttcacgtttttt-3'

MAP3K10

SEQ ID NO:81 5'-tcctcctccatgggggaggg-3'
SEQ ID NO:82 5'-ctcctccatgggggaggggc-3'
SEQ ID NO:83 5'-cctccatgggggaggggccg-3'

BAX-beta

SEQ ID NO:84 5'-gaccggtccatcaccgccgc-3'
SEQ ID NO:85 5'-cccgtccatcaccgccgctc-3'
SEQ ID NO:86 5'-cgtccatcaccgccgctccc-3'

KCNMA1

SEQ ID NO:87 5'-ccatttgccatagctagcaa-3'
SEQ ID NO:88 5'-atttgccatagctagcaacg-3'
SEQ ID NO:89 5'-ttgccatagctagcaacggg-3'

FAK2

SEQ ID NO:90 5'-accccagacatcctctcagg-3'
SEQ ID NO:91 5'-cccagacatcctctcaggca-3'
SEQ ID NO:92 5'-cagacatcctctcaggcagc-3'

ABCC8

SEQ ID NO:93 5'-gccaggggcatggcggcgcg-3'
SEQ ID NO:94 5'-caggggcatggcggcgcggg-3'
SEQ ID NO:95 5'-ggggcatggcggcgcgggcg-3'

PDE9A

SEQ ID NO:96 5'-ccggatcccatcctgcgccc-3'
SEQ ID NO:97 5'-ggatcccatcctgcgcccgg-3'
SEQ ID NO:98 5'-atcccatcctgcgcccggcg-3'

SCD

SEQ ID NO:99 5'-tgggccggcatcttggtct-3'
SEQ ID NO:100 5'-ggccggcatcttggtctcc-3'
SEQ ID NO:101 5'-ccggcatcttggtctccga-3'

RAB11A

SEQ ID NO:102 5'-cgggtgcccattgcgcggcc-3'

SEQ ID NO:103 5'-ggtgcccattgcgcggccga-3'

SEQ ID NO:104 5'-tgcccattgcgcggccgagg-3'

FAK

SEQ ID NO:105 5'-gcagctgccattattttgct-3'

SEQ ID NO:106 5'-agctgccattattttgctag-3'

SEQ ID NO:107 5'-ctgccattattttgctagat-3'

CSNK2A2

SEQ ID NO:108 5'-gggccgggcatggcgggcgg-3'

SEQ ID NO:109 5'-gccgggcatggcgggcggga-3'

SEQ ID NO:110 5'-cgggcatggcgggcgggacc-3'

GTM3

SEQ ID NO:111 5'-atagacgactcgcacgacat-3'

SEQ ID NO:112 5'-tgtgcggaaatccattactt-3'

SEQ ID NO:113 5'-actgggccatcttggtgttg-3'

BCR

SEQ ID NO:114 5'-gggtccaccatggcgcggcc-3'

SEQ ID NO:115 5'-gtccaccatggcgcggccgg-3'

SEQ ID NO:116 5'-ccaccatggcgcggccggcc-3'

PSD95

SEQ ID NO:117 5'-agacagtccatggtgggggg-3'

SEQ ID NO:118 5'-acagtccatggtggggggcc-3'

SEQ ID NO:119 5'-agtccatggtggggggcctg-3'

DLG3

SEQ ID NO:120 5'-tgcttgatgcatggcactgcc-3'

SEQ ID NO:121 5'-cttgatgcatggcactgcccc-3'

SEQ ID NO:122 5'-tgtgcatggcactgcccccc-3'

SEMA4C(821)

SEQ ID NO:123 5'-tgtggggccatggcgacgc-3'

SEQ ID NO:124 5'-tggggccatggcgacgccc-3'

SEQ ID NO:125 5'-ggggccatggcgacgccccg-3'

HTF4

SEQ ID NO:126 5'-tggggattcatcttcggcca-3'

SEQ ID NO:127 5'-gggattcatcttcggccact-3'

SEQ ID NO:128 5'-gattcatcttcggccacttc-3'

SRCAP

SEQ ID NO:129 5'-tccttgggccatggtggaagc-3'

SEQ ID NO:130 5'-cttgggccatggtggaagcaa-3'

SEQ ID NO:131 5'-tgggccatggtggaagcaatt-3'

FKBP25

SEQ ID NO:132 5'-gccgccgccatcttccggat-3'

SEQ ID NO:133 5'-cgccgccatcttccggattt-3'

SEQ ID NO:134 5'-ccgccatcttccggatttta-3'

APP(695)

SEQ ID NO:135 5'-ccgggcagcatcgcgaccct-3'

SEQ ID NO:136 5'-gggcagcatcgcgaccctgc-3'

SEQ ID NO:137 5'-gcagcatcgcgaccctgcgc-3'

AP3D1

SEQ ID NO:138 5'-ttgagggccatcgcggcggc-3'

SEQ ID NO:139 5'-gagggccatcgcggcggccc-3'

SEQ ID NO:140 5'-gggccatcgcggcggcccac-3'

PTPZ

SEQ ID NO:141 5'-aggattcgcatcttccagacg-3'

SEQ ID NO:142 5'-gattcgcatcttccagacggt-3'

SEQ ID NO:143 5'-ttcgcatcttccagacggtct-3'

PGD-synt

SEQ ID NO:144 5'-tgagtagccattctcctgca-3'

SEQ ID NO:145 5'-agtagccattctcctgcagc-3'

SEQ ID NO:146 5'-tagccattctcctgcagcag-3'

ACHE(614)

SEQ ID NO:147 5'-gggggcctcatggctgcagg-3'

SEQ ID NO:148 5'-gggcctcatggctgcagggc-3'

SEQ ID NO:149 5'-gcctcatggctgcagggcag-3'

CAPN4

SEQ ID NO:150 5'-accaggaacatggctgcgac-3'

SEQ ID NO:151 5'-caggaacatggctgcgactc-3'

SEQ ID NO:152 5'-ggaacatggctgcgactcac-3'

KIAA0436

SEQ ID NO:153 5'-aatgcatccatgttttctgg-3'

SEQ ID NO:154 5'-tgcacatccatgttttctggaa-3'

SEQ ID NO:155 5'-catccatgttttctggaagg-3'

ALPEND

SEQ ID NO:156 5'-ttctgggacatggcgggacc-3'

SEQ ID NO:157 5'-ctgggacatggcgggaccgg-3'

SEQ ID NO:158 5'-gggacatggcgggaccggga-3'

GIPC

SEQ ID NO:159 5'-cccagcggcatgagcagcga-3'

SEQ ID NO:160 5'-cagcggcatgagcagcgaga-3'

SEQ ID NO:161 5'-gcggcatgagcagcgagaag-3'

CTNND2

SEQ ID NO:162 5'-ggcggcttcctcgcaaaca-3'

SEQ ID NO:163 5'-attggcattttgagtgcac-3'

SEQ ID NO:164 5'-gccgggtagtggtcgcttc-3'

CLTC

SEQ ID NO:165 5'-atctgggccatggcgctgtc-3'

SEQ ID NO:166 5'-ctgggccatggcgctgtcgg-3'

SEQ ID NO:167 5'-gggccatggcgctgtcgggg-3'

PKP2 (881)

SEQ ID NO:168 5'-ggggctgccatggggccggt-3'

SEQ ID NO:169 5'-ggctgccatggggccggtgg-3'

SEQ ID NO:170 5'-ctgccatggggccggtgggg-3'

14-3-3b-1

SEQ ID NO:171 5'-tccattgtcattccctgact-3'

SEQ ID NO:172 5'-cattgtcattccctgactcc-3'

SEQ ID NO:173 5'-ttgtcattccctgactccaa-3'

14-3-3z

SEQ ID NO:174 5'-tttttatccatgactggatg-3'

SEQ ID NO:175 5'-tttatccatgactggatgtt-3'

SEQ ID NO:176 5'-tatccatgactggatgttct-3'

EPS8

SEQ ID NO:177 5'-tgaccattcattgtgtcttt-3'

SEQ ID NO:178 5'-accattcattgtgtctttca-3'

SEQ ID NO:179 5'-cattcattgtgtctttcact-3'

SNCA(140)

SEQ ID NO:180 5'-aatacatccatggctaata-3'

SEQ ID NO:181 5'-tacatccatggctaata-3'

SEQ ID NO:182 5'-catccatggctaata-3'

ERAB

SEQ ID NO:183 5'-ctccgacacgctgctgcat-3'

SEQ ID NO:184 5'-tgacccacgctggcctccc-3'

SEQ ID NO:185 5'-ctgcatacgaatggcccat-3'

Bcl2-alpha

SEQ ID NO:186 5'-gcgtgcgccatccttcccag-3'

SEQ ID NO:187 5'-gtgcgccatccttcccagag-3'

SEQ ID NO:188 5'-gcgccatccttcccagagga-3'

ENOA

SEQ ID NO:189 5'-agaatagacatggtgaactt-3'

SEQ ID NO:190 5'-aatagacatggtgaacttct-3'

SEQ ID NO:191 5'-tagacatggtgaacttctag-3'

AXIN

SEQ ID NO:192 5'-tggtggcgggaccccgggcc-3'

SEQ ID NO:193 5'-tgacacggccctgggggccc-3'

SEQ ID NO:194 5'-ctcgaacctcctcaaacc-3'

cit-synt

SEQ ID NO:195 5'-gccgcagtaagtaaagccat-3'

SEQ ID NO:196 5'-gttagagtcaatggcccca-3'

SEQ ID NO:197 5'-gctcatggacttgggccttt-3'

ALDOC

SEQ ID NO:198 5'-gagtgaggcatggtgacagc-3'

SEQ ID NO:199 5'-gtgaggcatggtgacagctc-3'

SEQ ID NO:200 5'-gaggcatggtgacagctccc-3'

CKB

SEQ ID NO:201 5'-gagaagggcatggcggcggc-3'

SEQ ID NO:202 5'-gaagggcatggcggcggcgg-3'

SEQ ID NO:203 5'-agggcatggcggcggcgggc-3'

NRGN

SEQ ID NO:204 5'-cagcagtccatgctggtgtc-3'

SEQ ID NO:205 5'-gcagtccatgctggtgtcgg-3'

SEQ ID NO:206 5'-agtccatgctggtgtcgggg-3'

RAB3A

SEQ ID NO:207 5'-gcggatgccatcttgccctg-3'

SEQ ID NO:208 5'-ggatgccatcttgccctgca-3'

SEQ ID NO:209 5'-atgccatcttgccctgcacc-3'

PRDX3

SEQ ID NO:210 5'-cgtcctacagcagccgcat-3'

SEQ ID NO:211 5'-accaaataatttccccttaaa-3'

SEQ ID NO:212 5'-cttctgaaagtactctttgg-3'

SMN1

SEQ ID NO:213 5'-ctcatcgccatagcaaacc-3'

SEQ ID NO:214 5'-catcgccatagcaaaccgc-3'

SEQ ID NO:215 5'-tcgccatagcaaaccgcgg-3'

SFRS9

SEQ ID NO:216 5'-cagcccgacatccgcaccgc-3'

SEQ ID NO:217 5'-gcccgacatccgcaccgccc-3'

SEQ ID NO:218 5'-ccgacatccgcaccgcccga-3'

TFCP2

SEQ ID NO:219 5'-gcccaggccatcctggctcc-3'

SEQ ID NO:220 5'-ccaggccatcctggctcctt-3'

SEQ ID NO:221 5'-aggccatcctggctccttcc-3'

4F5S

SEQ ID NO:222 5'-ccacgggccatgccgaccac-3'

SEQ ID NO:223 5'-acgggccatgccgaccacca-3'

SEQ ID NO:224 5'-gggccatgccgaccaccaac-3'

Peptide Fragments

Of BAT3 Interactors:

GLYP

SEQ ID NO:225 CSEKMALSTASDDRCWNGMA

SEQ ID NO:226 RGRYLPEVMGDGLANQINNP

SEQ ID NO:227 EVEVDITKPDMTIRQQIMQL

SEQ ID NO:228 KIMTNRLRSAYNGNDVDFQD

SEQ ID NO:229 TNRLRSAYNGNDVDFQDASD

SEQ ID NO:230

CSEKMALSTASDDRCWNGMARGRYLPEVMGDGLANQINNPEVEVDITKPD

SEQ ID NO:231

DGLANQINNPEVEVDITKPDMTIRQQIMQLKIMTNRLRSAYNGNDVDFQD

LRP2

SEQ ID NO:232 MDRGPAAVACTLLLALVACL

SEQ ID NO:233 GCAVVTCQQGYFKCQSEGQC

SEQ ID NO:234 IPSEYRCDHVRDCPDGADEN

SEQ ID NO:235 CNYPTCGGYQFTCPSGRCIY

SEQ ID NO:236 SDERQDCSQSTCSSHQITCS

SEQ ID NO:237

TLLLALVACLAPASGQECDSAHRFCGSGHCI PADWRCDGTKDCSDDADEI

SEQ ID NO:238

RDCPDGADENDCQYPTCEQLTCDNGACYNTSQKCDWKVDCRDSSDEINCT

LRPAP1

SEQ ID NO:239 RGLPALLLLLLFLGPWPAAS

SEQ ID NO:240 QLWEKAQRLHLPPVRLAELH

SEQ ID NO:241 KYGLDGKKDARQVTSNSLSG

SEQ ID NO:242 EKVHEYNVLLETLSRTEEIH

SEQ ID NO:243 VSHQGYSTEAEFEEPRVIDL

SEQ ID NO:244

AHEKLRHAESVGDGERVSRREKHALLGRTKELGYTVKKHLQDLSGRIS

SEQ ID NO:245

ARQVTSNSLSGTQEDGLDDPRLEKLWHKAKTSGKFSGEELDKLWREFLHH

TTR

SEQ ID NO:246 LLLCLAGLVFVSEAGPTGT
SEQ ID NO:247 WEPFASGKTSESGELHGLTT
SEQ ID NO:248 EEEFVEGIYKVEIDTKSYWK
SEQ ID NO:249 ALGISPFHEHAEVVFTANDS
SEQ ID NO:250 GPRRYTIAALLSPYSYSTTA
SEQ ID NO:251
LLCLAGLVFVSEAGPTGTGESKCPLMVKVLDAVRGSPAINVAVHVFRKAA
SEQ ID NO:252
ESGELHGLTTEEEFVEGIYKVEIDTKSYWKALGISPFHEHAEVVFTANDS

AP3D1

SEQ ID NO:253 LESGDLSMSSIKVDGIRMSF
SEQ ID NO:254 QNLLAKICFHHHFSVVERVD
SEQ ID NO:255 SCASMYRSIQGHHVCLLVK
SEQ ID NO:256 KGENSVSVDGKCSDESTLLSN
SEQ ID NO:257 SDSTLLSNLLEEMKATLAKC
SEQ ID NO:258
NLLAKICFHHHFSVVERVDSCASMYRSIQGHHVCLLVKKGGENSVSVDGK

Of APBB1(710) Interactors:**PN7740**

SEQ ID NO:259 WDNFGIWDNRIDEPIILLPPS
SEQ ID NO:260 LYFAVYDGHGGPAAADFCHT
SEQ ID NO:261 ATLLTSGTTATVALLRDGIE
SEQ ID NO:262 GGFVAWNSLGQPHVNGRLAM
SEQ ID NO:263 NFMVNSQEICDFVNQCHDPN
SEQ ID NO:264
LLQDDRRVTPTCHSSTSEPRCSRFPDGS GPATWDNFGIWDNRIDEPI
SEQ ID NO:265
GQPHVNGRLAMTRSIGDLDLKTSGVIAEPETKRIKLHHADDSFLVLTTDG

Of APBA1 Interactors:**GLUL**

SEQ ID NO:266 RTLDSEPKCVEELPEWNFDG
SEQ ID NO:267 SSTLQSEGSNSDMYLVPAAM
SEQ ID NO:268 MDMVSNQHPWFGMEQEYTLM
SEQ ID NO:269 RACLYAGVKIAGTNAEVMIPA
SEQ ID NO:270 FPGPQGPYYCGVGADRAYGR
SEQ ID NO:271
LQSEGSNSDMYLVPAAMFRDPFRKDPNKLVLCEVFKYNRRPAETNLRHTC
SEQ ID NO:272
HPWFGMEQEYTLMGTDGHPFGWPSNGFPGPQGPYYCGVGADRAYGRDIVE

KIAA0472

SEQ ID NO:273 TTPQONKMDKLEILNSMR
SEQ ID NO:274 AVSDRSFAFTAALKCDKMAL
SEQ ID NO:275 LCEVFGTMRSTGEPFRVLV
SEQ ID NO:276 EMMTELLASARDKMLCPSES
SEQ ID NO:277 EVIELHANSWNPLTPPITQY
SEQ ID NO:278
FTAAKLCDKMALFMVEGTKFRSLLLNLQKDFTVREELQQQDVERWLGFI
SEQ ID NO:279
RSSTGEPFRVLVCPIYTCLRELLQSQDVKEDAVLCCSMELQSTGRLLLEEQ

Of PS1(467) Interactors:**APBA1**

SEQ ID NO:280 VRMMQAEAVSRIKMAQKLA
SEQ ID NO:281 PLRTISYIADIGNIVVLMAR
SEQ ID NO:282 AQSIGQAFSVAYQEFLRANG
SEQ ID NO:283 KQKGEILGVVIVESGWGSIL
SEQ ID NO:284 TCQSIKGLKNQSRVKLNIV
SEQ ID NO:285
ADIGNIVVLMARRRMPRSNSQENVEASHPSQDGKRQYKMICHVFESDAQ
SEQ ID NO:286
GVVIVESGWGSILPTVIIANMMHGGPAEKSGKLNIGDQIMSINGTSLVGL

PGAD

SEQ ID NO:287 MAFANLRKVLISDSLDPCCR
SEQ ID NO:288 QNLSKEELIAELQDCEGLIV
SEQ ID NO:289 ADVINAAEKLQVVGRAGTGV
SEQ ID NO:290 LVMNTPNGNSLSAAELTCGM
SEQ ID NO:291 DEGALLRALQSGQCAGAALD
SEQ ID NO:292
QATASMKGDKWERKKFMGTENGLGILGLGRIGREVATRMQSFGMKTI
SEQ ID NO:293
SASFGVQQPLLEEIWPLCDFITVHTPLLPSTTGLLNDNTFAQCKKGVRVV

ETFB

SEQ ID NO:294 TDGVKHSMPFCEIAVEEAV
SEQ ID NO:295 VIAVSCGPAQCQETIRTALA
SEQ ID NO:296 LLGKQAIDDDCNQTGQMTAG
SEQ ID NO:297 VTADLRLNEPRYATLPNIMK
SEQ ID NO:298 AERLGPLQVARVLAKLAEKE
SEQ ID NO:299
DDCNQTGQMTAGFLDWPQGTFFASQVTLEGDKLKVEREIDGGLETLRLKLP
SEQ ID NO:300
PRYATLPNIMKAKKKKIEVIKPGDLGVDLTSKLSVISVEDPPQRTAGVKV

GAPD

SEQ ID NO:301 GKVKVGVNGFGRIGRLVTRAAFNS
SEQ ID NO:302 KAENGKLVINGNPITIFQERD
SEQ ID NO:303 ISAPSADAPMFVMGVNHEKY
SEQ ID NO:304 DNSLKIISNASCTTNCLAPL
SEQ ID NO:305 AKVIHDNFGIVEGLMTTVHA
SEQ ID NO:306
FGRIGRLVTRAAFNSGKVDIVAINDPFIDLNYMVYMFQYDSTHGKFHGT
SEQ ID NO:307
NGNPITIFQERDPSKIKWGDAGAIEYVVESTGVFTTMEKAGAHLQGGAKRV

FKBP25

SEQ ID NO:308 VGVGKVIRGWDEALLTMSKG
SEQ ID NO:309 EKARLEIEPEWAYGKKGQPD
SEQ ID NO:310 DAKIPPAKLTFEVELVDID
SEQ ID NO:311
VIRGWDEALLTMSKGEKARLEIEPEWAYGKKGQPD
AKIPPAKLTFEVEL

RAB11A

SEQ ID NO:312 LKELRDHADSNIIVIMLVGNK
SEQ ID NO:313 SDLRHLRAVPTDEARAFAEK
SEQ ID NO:314 NGLSFIETSALDSTNVEAAF
SEQ ID NO:315 QTILTEIYRIVSQKQMSDRR
SEQ ID NO:316 ENDMSPSNVPIHVPPTTE
SEQ ID NO:317
TILTEIYRIVSQKQMSDRRENDMSPSNVPIHVPPTTENKPKVQCCQNI
SEQ ID NO:318
LKELRDHADSNIIVIMLVGNKSDLRHLRAVPTDEARAFAEKNGLSFIETSA

ENOA

SEQ ID NO:319 ADLAGNSEVILPVPAFNVIN
SEQ ID NO:320 AMRIGAEVYHNLKNVIKEY
SEQ ID NO:321 KEGLELLKTAIGKAGYTDKV
SEQ ID NO:322 VIGMDVAASEFFRSGKYDLD
SEQ ID NO:323 KSFIDYPVVSIEDPFDQDD
SEQ ID NO:324
WQKFTASAGIQVVGDDLTVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTES
SEQ ID NO:325
QANGWGMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQL

TFCP2

SEQ ID NO:326 QQQQQQQQKHEDGDSNGTF
SEQ ID NO:327 NGTFFVYHAIYLEELTAVEL
SEQ ID NO:328 TEKIAQLFSISPCQISQIYK
SEQ ID NO:329 QGPTGIHVLISDEMIQNFQE
SEQ ID NO:330 EACFILDITMKQETNDSYHII

SEQ ID NO:331
QQQQQQQQKHEDGDSNGTFFVYHAIYLEELTAVELTEKIAQLFSISPCQ
SEQ ID NO:332
CQISQIYKQGPTGIHVLISDEMIQNFOEEACFILD TMKQETNDSYHIILK

Of PS2(448) Interactors:

GAPD

SEQ ID NO:333 GKVKVGVNGFGRIGRLVTRA
SEQ ID NO:334 AINDPFIDLNYMVYMFQYDS
SEQ ID NO:335 KAENGKLVINGNPITIFQER
SEQ ID NO:336 ISAPSADAPMFVMGVNHEKY
SEQ ID NO:337 ITATQKTVDGPSGKLWRDGR
SEQ ID NO:338
GNPITIFQERDPSKIKWGDAGAEYVVESTGVFTTMEKAGAH LQGGAKRVI
SEQ ID NO:339
MFVMGVNHEKYDNSLKIISNASCTTNCLAPLAKVIHDNFGIVEGLMTTVH

Of CASK Interactors:

DMD(3685)

SEQ ID NO:340 KLSIPQLSVTDYEIMEQRLG
SEQ ID NO:341 EFEEIEGRWKKLSSQLVEHC
SEQ ID NO:342 SEILKKQLKQCRLLVSDIQT
SEQ ID NO:343 MCQQVYARKEALKGGLEKT
SEQ ID NO:344 KRAKEEAQQKEAKVKLLTES
SEQ ID NO:345
VAQEALKKELETLTNYQWLCTRLNGKCKTLEEVWACWHELLSYLEKANK
SEQ ID NO:346
ADFVAFTNHFQVFSQVQAREKELQTFDTLPPMRYQETMSAIRTWVQQS

Of CIB Interactors:

S1P

SEQ ID NO:347 MKQALIASARRLPGVNMFEQ
SEQ ID NO:348 QASLSPSYIDLTECPYMWPY
SEQ ID NO:349 NGDNIEVAFSYSSVLWPWSG
SEQ ID NO:350 EQTSTVKLPIKVKIIPTPR
SEQ ID NO:351 QGHGKLDLLRAYQILNSYKP
SEQ ID NO:352
IDLTECPYMWPYCSQPIYYGGMPTVVNVITILNGMGVTGRIVDKPDWQPYL
SEQ ID NO:353
NGDNIEVAFSYSSVLWPWSGYLAISISVTKKAASWEGIAQGHVMITVASP

ATPMB

SEQ ID NO:354 ADDLTD PAPATTF AHL DATT
SEQ ID NO:355 NIVGSEHYDVARGVQKILQD
SEQ ID NO:356 YKSLQDI IAILGMDELSEED
SEQ ID NO:357 KLT VSRARKIQRFLSQPFQV
SEQ ID NO:358 VAEVFTGHMGKLVPLKETIK
SEQ ID NO:359
ADDLTD PAPATTF AHL DATT VLSRAIAELGIYPAVDPLDSTSRIMDPNIV
SEQ ID NO:360
ILGMDELSEEDKLT VSRARKIQRFLSQPFQVAEVFTGHMGKLVPLKETIK

MAP3K10

SEQ ID NO:361 EIDALAVAYGVAMNKLTLPI
SEQ ID NO:362 EQSALFQMPLESFHS LQEDW
SEQ ID NO:363 RREQELAE REMDIVERELHL
SEQ ID NO:364 EHKITVQASPTLDRKKGSDG
SEQ ID NO:365 SSSGGSGTWSRGGPPKKEEL
SEQ ID NO:366
LESFHS LQEDWKLEIQHMFDDLRTKEKELRSREEELLRAAQEQRFQEEQL
SEQ ID NO:367
PTLDRKKGSDGASPPASPSII PRLRAIRLTPVDCGGSSSGSSSGSGTWS

SCD

SEQ ID NO:368 HHSFPYDYSASEYRWHINFN
SEQ ID NO:369 TFFIDWMAALGLTYDRKKVS
SEQ ID NO:370 SKAAILARIKRTGDGNYKSG
SEQ ID NO:371 ASEYRWHINFNTFFIDWMAA
SEQ ID NO:372 TYDRKKVSKAAILARIKRTG
SEQ ID NO:373
HHSFPYDYSASEYRWHINFNTFFIDWMAALGLTYDRKKVSKAAILARIKR
SEQ ID NO:374
ASEYRWHINFNTFFIDWMAALGLTYDRKKVSKAAILARIKRTGDGNYKSG

Of APBA2 Interactors:**S1P**

SEQ ID NO:375 DTGGANIPALNELLSVWNMG
SEQ ID NO:376 ANHDMYYASGCSI AKFPEDG
SEQ ID NO:377 IVLYGDSNCLDDSHRQKDCF
SEQ ID NO:378 EGNHLHRYSKVLEAHLGDPK
SEQ ID NO:379 PLNETAPSNLWKHQKLLSID
SEQ ID NO:380
GCSI AKFPEDGVVITQT F KDQGLEVLKQETAVVENVPILGLYQIPAE GGG

SEQ ID NO:381
DDSHRQKDCFWLLDALLQYTSYGVTPPSLSHSGNRQRPPSGAGSVTPERM

PDE9A

SEQ ID NO:382 CVHDNYRNNPFHNFRHCFCV
SEQ ID NO:383 NTYQINARTELAVRYNDISP
SEQ ID NO:384 LATDMARHAEIMDSFKEKME
SEQ ID NO:385 LEEYFMQSDREKSEGLPVAP
SEQ ID NO:386 QPLWESRDRYEELKRIDDAM
SEQ ID NO:387
NEMLSCLEHMYHDLGLVRDFSINPVTLLRRWLCVHDNYRNNPFHNFRHCF
SEQ ID NO:388
DREKSEGLPVAPFMDRDKVTKATAQIGFIKFVLIPMFETVTKLFPMVEEI

Of GASP Interactors:

PI4K

SEQ ID NO:389 SELEKEGLRCRSDSEDECST
SEQ ID NO:390 FKVGDDCRQDMLALQIIDLF
SEQ ID NO:391 GRQTDFGMYDYFTRQYGDDES
SEQ ID NO:392 GHIIHIDFGFMFESSPGGNL
SEQ ID NO:393 PYMDAVVSLVTLMLDTGLPC
SEQ ID NO:394
YDYFTRQYGDESTLAFQQARYNFIRSMAAYSLLLFLQIKDRHNGNIMLD
SEQ ID NO:395
FMFESSPGGNLGWEPDIKLTDEMVMIMGGKMEATPFKWFMEMCVRGYLAV

5HT-2A

SEQ ID NO:396 YSNDFNSGEANTSDAFNWTV
SEQ ID NO:397 LSPSCLSLHLQEKNEWSALL
SEQ ID NO:398 TAVVIILTIAGNILVIMAVS
SEQ ID NO:399 LEKKLQNATNYFLMSLAIAD
SEQ ID NO:400 LMSLAIADMLLGFLVMPVSM
SEQ ID NO:401
LYSNDFNSGEANTSDAFNWTVDSENRTNLSCEGCLSPSCLSLHLQEKNW
SEQ ID NO:402
ALLTAVVIILTIAGNILVIMAVSLEKKLQNATNYFLMSLAIADMLLGFLV

Of KIAA0351 Interactors:

TRIO(2861)

SEQ ID NO:403 VIHEVLHHQRHVRTIWQHRK
SEQ ID NO:404 LHRARALQKRHEDFEEVAQN
SEQ ID NO:405 VRRVEQRKILLDMSVSFHTH

SEQ ID NO:406 TLQVTNVNVIKEGEDLIQQLR
SEQ ID NO:407 ELFQERKIKLELFLHVRIFE
SEQ ID NO:408
QKRHEDFEEVAQNITYTNADKLLAEAEQLAQTGECDPEEIYQAAHQLEDRI
SEQ ID NO:409
KEGEDLIQQLRDSAISSNKTPHNSSINHIE TVLQQLDEAQSQMEELFQER

Of BAX-beta Interactors:

KCNMA1

SEQ ID NO:410 RILINPGNHLKIQEGTLGFF
SEQ ID NO:411 IASDAKEVKRAFFYCKACHD
SEQ ID NO:412 DITDPKRIKKCGCKRLEDEQ
SEQ ID NO:413 PSTLSPKKKQRNGGMRNSPN
SEQ ID NO:414 TSPKLMRHDPLLPNDQID
SEQ ID NO:415
IITELVNDTNVQFLDQDDDDPDTELYLTQPFACGTAFVSVLDSLMSAT
SEQ ID NO:416
VSILPGTPLSRADLRAVNINLCDCMVILSANQNNIDDTSLQDKECILASL

Of FAK2 Interactors:

ABCC8

SEQ ID NO:417 VVYYHNIETSNFPKLLIALL
SEQ ID NO:418 MLLLEVNVRVRRYIFFKT
SEQ ID NO:419 PREVKPPEDLQDLGVRFLQP
SEQ ID NO:420 FVNLLSKGTYWWMNAFIKTA
SEQ ID NO:421 HKKPIDLRAIGKLPIAMRAL
SEQ ID NO:422
VVYYHNIETSNFPKLLIALLVYWTAFITKTIKFVKFLDHAIGFSQLRFC
SEQ ID NO:423
RFLQPFVNLLSKGTYWWMNAFIKTAHKKPIDLRAIGKLPIAMRALTNYQR

Of RAB11A Interactors:

FAK

SEQ ID NO:424 EMEEDQRWLEKEERFLKPDVR
SEQ ID NO:425 RGSIDREDGSLQGPIGNQHIYQPVG
SEQ ID NO:426 GVKLQPQEISPPPTANLDRSNDKVY
SEQ ID NO:427 LRTLLATVDETIPLLPASTHRE
SEQ ID NO:428 LNSDLGELINKMKLAQQYVMTSLQ
SEQ ID NO:429
GSLQGPIGNQHIYQPVGKPDPAAPPKKPPRPGAPGHLGSLASLSSPADSY

SEQ ID NO:430
PPPTANLDRSNDKVYENVVTGLVKAVIEMSSKIQPAPPEEYVPMVKEVGLA

Of FAK Interactors:

CSNK2A2

SEQ ID NO:431 IDLDPHFNDILGQHSRKRWE
SEQ ID NO:432 NFIHSENRLVLSPEALDLLD
SEQ ID NO:433 KLLRYDHQQRLTAKEAMEHP
SEQ ID NO:434 YFYPVVKEQSQPCADNAVLS
SEQ ID NO:435 EQSQPCADNAVLSGLTAAR
SEQ ID NO:436
IDLDPHFNDILGQHSRKRWENFIHSENRLVLSPEALDLLDKLLRYDHQQR
SEQ ID NO:437
LLDKLLRYDHQQRLTAKEAMEHPYFYPVVKEQSQPCADNAVLSGLTAAR

GTM3

SEQ ID NO:438 AHAI RLLLEFTDTSYEEKRY
SEQ ID NO:439 YLLDGKNKITQSNAILRYIA
SEQ ID NO:440 EKLKPQYLEELPGQLKQFSM
SEQ ID NO:441 EKLKPQYLEELPGQLKQFSM
SEQ ID NO:442 SMCKMPINNMAQWGNKPVC
SEQ ID NO:443
GKNKITQSNAILRYIARKHNMCGETEEEEKIRVDI IENQVMDFR TQLIRLC
SEQ ID NO:444
QYLEELPGQLKQFSMFLWKFSWFAGEKLT FVDFLT YDILDQNRIFDPKCL

Of BCR Interactors:

PSD95

SEQ ID NO:445 LRVNDSILFVNEVDVREVTH
SEQ ID NO:446 NEVDVREVTHSAAVEALKEA
SEQ ID NO:447 QHIPGDNSIYVTKIIEGGAA
SEQ ID NO:448 LKVAKPSNAYLSDSYAPPDI
SEQ ID NO:449 PAEKVMEIKLIKGPGLGFS
SEQ ID NO:450
REVTHSAAVEALKEAGSIVRLYVMRRKPPAEKVMEIKLIKGPGLGFSIA
SEQ ID NO:451
IYVTKIIEGGAHKDGR LQIGDKILAVNSVGL EDVMHEDAVAALKNTYDV

DLG3

SEQ ID NO:452 STPKLNGSGPSWWPECTCTN
SEQ ID NO:453 NGSDGMFKYEEIVLERGNSG
SEQ ID NO:454 DCVLRVNEVEVSEVVHSRAV
SEQ ID NO:455 FITKIIPGGAAAMDGR LGVN

SEQ ID NO:456 TSDMVYLKVAKPGSLHLNDM
SEQ ID NO:457
PPTRYSPIPRHMLAEEDFTREPRKII LHKGSTGLGFNIVGGEDGEGIFVS
SEQ ID NO:458
DLSGELRRGDRILSVNGVNLNRNATHEQAAAALKRAGQSVTIVAQYRPEEY

SEMA4C (821)

SEQ ID NO:459 LVLSLRRRLREELEKGAKAT
SEQ ID NO:460 ATERTLVYPLELPKEPTSPP
SEQ ID NO:461 FRPCPEPDEKLWDPVGYYYYS
SEQ ID NO:462 DGSLKIVPGHARCQPGGGPP
SEQ ID NO:463 SPPPGIPGQPLPSPTLHLG
SEQ ID NO:464
SNANGYVRLQLGGEDRGGLGHPLPELADELRRKLQQRQPLPDSNPPEESSV
SEQ ID NO:465
YYYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLPSPTLHLGGGRNSN

HTF4

SEQ ID NO:466 SFHRGSTSSSPYVAASHTPP
SEQ ID NO:467 INGSDSILGTRGNAAGSSQT
SEQ ID NO:468 GDALGKALASIYSPDHTSSS
SEQ ID NO:469 FPSNPSTPVGSPSPLTGTSQ
SEQ ID NO:470 WPRPGGQAPSSPSYENSLHS
SEQ ID NO:471
LQSRMEDRLDRLDDAIHVLNRNHAVGPSTSLPAGHSDIHSLLGPSHNAPIG
SEQ ID NO:472
GSLNSNYGGSSLVASSRSASMGVTHREDSVSLNGNHSVLSSTVTTSSDDL

SRCAP

SEQ ID NO:473 NILKKANQKRMLGDMAIEGG
SEQ ID NO:474 NFFTAYFKQQTIRELFDMP
SEQ ID NO:475 EEPSSSSVPSAPEEEEEETVA
SEQ ID NO:476 SKQTHILEQALCRAEDEEDI
SEQ ID NO:477 RAATQAKAEQVAELAEFNEN
SEQ ID NO:478
DGFPAGEGEEAGRPGAEDDEMSRAEQEIAALVEQLTPIERYAMKFLEASL
SEQ ID NO:479
AEQEIAALVEQLTPIERYAMKFLEASLEEVSRLEELKQAEQVEAARKDLD

Of FKBP25 Interactors:

CIB

SEQ ID NO:480 MGGSGSRLSKELLA EYQDLT
SEQ ID NO:481 FLTKQEILLAHRRFCCELLPQ
SEQ ID NO:482 EQRSVESSLRAQVPFEQILS
SEQ ID NO:483 LPELKANPFKERICRVFSTS

SEQ ID NO:484 PAKDSLSEFEDFLDLLSVFSD
SEQ ID NO:485
TATPDIKSHYAFRIFDFDDDGTLNREDLSRLVNCLTGEGEDTRLSASEMK
SEQ ID NO:486
TRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASSFKIVL

Of APP(695) Interactors:

BAT3

SEQ ID NO:487 ADLQFSQLLGNLLGPAGPGA
SEQ ID NO:488 PPPPPPPPAPEQQTMPPPGS
SEQ ID NO:489 GSSESIAAFIQRLSGSSNIF
SEQ ID NO:490 LQPQLRSFFHQHYLGGQEPT
SEQ ID NO:491 FLQEQFNSIAAHVLHCTDSG
SEQ ID NO:492
QDIQSQRKVKPQPPLSDAYLSGMPAKRRKTMQGEQGPQLLLSEAVSRAAKA
SEQ ID NO:493
VSWLTMMGLRLQVVLEHMPVGPDAILRYVRRVGDPPQPLPEEPMEVQGA

PTPZ

SEQ ID NO:494 PNMVDNVNKLNASLQETSVS
SEQ ID NO:495 ISSTKGMFPGSLAHTTTTKVF
SEQ ID NO:496 KVFDHEISQVPENNFVSVQPT

KIAA0351

SEQ ID NO:497 IDSAYPASGSIMENEQRSNQ
SEQ ID NO:498 MNNILRIIADLQVSCSYDHL
SEQ ID NO:499 DLAGPSAGSGSARFSRRPTC
SEQ ID NO:500 FPSEKARHLLDDSVLESRSP
SEQ ID NO:501 LGSSESSEFSEEMSSGLESP
SEQ ID NO:502
CSLGNSAAVPTMEGPLRRKTLLKEGRKPALSSWTRYWVILSGSTLLYYGA
SEQ ID NO:503
HYKSTPGKKVSIVGWMVQLPDDPEHPDIFQLNNPDKGNVYKFQTGSRFHA

PGD-synt

SEQ ID NO:504 ALSMCKSVVAPATDGGLNLT
SEQ ID NO:505 STFLRKNQCETRTMLLQPAG
SEQ ID NO:506 SLGSYSYRSPHWGSTYSVSV
SEQ ID NO:507 GRWFSAGLASNSSWLREKKA
SEQ ID NO:508 VETDYDQYALLYSQGSKGPG
SEQ ID NO:509
MATHHTLWMGLALLGVLDLQAAPEAQVSVQPNFQQDKFLGRWFSAGLAS
SEQ ID NO:510
EDFRMATLYSRTQTPRAELKEKFTAFCKAQGFTEDTIVFLPQTDKCMTEQ

Of ACHE(614) Interactors:

CAPN4

SEQ ID NO:511 MFLVNSFLKGGGGGGGGGGG
SEQ ID NO:512 GNVLGGLISGAGGGGGGGGGG
SEQ ID NO:513 ILGGVISAISEAAAQYNPEP
SEQ ID NO:514 ESEEVQRFRRLFAQLAGDDM
SEQ ID NO:515 MNILNKVVTRHPDLKTDGFG
SEQ ID NO:516
IDTCRSMVAVMDSDTTGKLGFEFEKYLWNNIKRWQAIYKQFDTDRSGTIC
SEQ ID NO:517
GFHLNEHLYNMIIRRYSDESGNMDFDNFISCLVRLDAMFRAFKSLDKDGT

KIAA0436

SEQ ID NO:518 HVIEDSHKKITAIKFLYEE
SEQ ID NO:519 KPQHYPsiHITAYENDERVP
SEQ ID NO:520 NSNPVLVRAVTLAPFLDVL
SEQ ID NO:521 RGGGELGLQWHADGRLTKKL
SEQ ID NO:522 SKDGKLVPMTVFHKTDSIDL
SEQ ID NO:523
ACGFIMDTNSDPKNCPPQLCSPIRPPKYTYKFAEGKLFEETGHEDPITK
SEQ ID NO:524
MNWDLFFTMKRNTKVIDLDMFKDHCVLFLKHSNLLYVNVIGLADDSVRS

ALPEND

SEQ ID NO:525 KEGILPERAEEAKLKAKYPS
SEQ ID NO:526 LGQKPGGSDFLMKRLQKGQK
SEQ ID NO:527 YFDSGDYNMAKAKMKNQLP
SEQ ID NO:528 SAGPDKNLVTGDHPTPQDL
SEQ ID NO:529 DLPQRKSSLVTSKLAGGQVE
SEQ ID NO:530
KEGILPERAEEAKLKAKYPSLGQKPGGSDFLMKRLQKGQKYFDSGDYNMA

GIPC

SEQ ID NO:531 GSPTGRIEGFTNVKELYGKI
SEQ ID NO:532 AEAFLPTAEVMFCTLNTHK
SEQ ID NO:533 VMDKLLGGQIGLEDFIFAH
SEQ ID NO:534 KEVEVFKSEDALGLTITDNG
SEQ ID NO:535 AFIKRIKEGSVIDHIHLISV
SEQ ID NO:536
QSLGCRHYEVARLLKELPRGRTFTLKLTEPRKAFDMISQRSAGGRPMSG
SEQ ID NO:537
ATVEDLPSAFEEKAIEKVDDLLESYMGIRDTELAATMVELGKDKRNPDEL

CTNND2

SEQ ID NO:538 LAAPQGGSPTKLQRGGSAP

SEQ ID NO:539 ATATLQRPGLAAGSRASYS
SEQ ID NO:540 RSLSQSQGVPLPPAHTGTyr
SEQ ID NO:541 ATFQRASYAAGPASNYADPY
SEQ ID NO:542 DNKIKAEIRRQGGIQLLVDL
SEQ ID NO:543
LWNLSLCDALKMPIIQDALAVLTNAVIIIPHSGWENSPLQDDRKIQLHSSQ
SEQ ID NO:544
SPGEEARRRMRECDGLTDALLYVIQSALGSSEIDSKTVENCVCILRNLSY

Of CTNND2 Interactors:

GIPC

SEQ ID NO:545 KKAPPLVENEEAEPRGGGLG
SEQ ID NO:546 GGGGSGGPQMGLPPPPPALR
SEQ ID NO:547 HGSPTGRIEGFTNVKELYGK
SEQ ID NO:548 TLNTHKVDMDKLLGGQIGLE
SEQ ID NO:549 SEDALGLTITDNGAGYAFIK
SEQ ID NO:550
NGQSLGCRHYEVARLLKELPRGRTFTLKLTEPRKAFDMISQRSAGGRPG
SEQ ID NO:551
RLRSRGPATVEDLPFAFEEKAIEKVDDLLESYMGIRDTELAATMVELGKD

CLTC

SEQ ID NO:552 AILYSKFQPKMREHLELFW
SEQ ID NO:553 AAEQAHLWAEVFLYDKYEE
SEQ ID NO:554 HPTDAWKEGQFKDIITKVAN
SEQ ID NO:555 FKPLLLNDLLMVLSPRLDHT
SEQ ID NO:556 PYLRVQNHNNKSVNESLNN
SEQ ID NO:557
EKRECFGACLFTCYDLLRPDVVLETAWRHNIMDFAMPYFIQVMKEYLTKV
SEQ ID NO:558
KEEEQATETQPIVYGQPQLMLTAGPSVAVPPQAPFGYGYTAPPYGPQPG

PKP2 (881)

SEQ ID NO:559 GSRSRKVKEQYQDVPMPEEK
SEQ ID NO:560 SNPKGVEWLWHSIVIRMYLS
SEQ ID NO:561 LIAKSVRNYTQEASLGALQN
SEQ ID NO:562 LTAGSGPMPTSV AQTVVQKE
SEQ ID NO:563 SGLQHTRKMLHVGDPSVKKT
SEQ ID NO:564
AISLLRNLSRNLSQLQNEIAKETLPDLVSIIPDTPSTDLLIETTASACYT
SEQ ID NO:565
MPEEKSNPKGVEWLWHSIVIRMYLSLIAKSVRNYTQEASLGALQNLTAGS

BCR

SEQ ID NO:566 ALKAAFDVNNKDVSVMMSEM
SEQ ID NO:567 DVNAIAGTLKLYFRELPEPL
SEQ ID NO:568 FTDEFYPNFAEGIALSDPVA
SEQ ID NO:569 KESCMLNLLLSLPEANLLTF
SEQ ID NO:570 LFLLDHLKRVAEKEAVNKMS
SEQ ID NO:571
TFLFLLDHLKRVAEKEAVNKMSLHNLATVFGPTLLRPSEKESKLPANPSQ
SEQ ID NO:572
ALKAAFDVNNKDVSVMMSEMDVNAIAGTLKLYFRELPEPLFTDEFYPNFA

14-3-3b(246)

SEQ ID NO:573 SELVQKAKLAEQAERYDDMA
SEQ ID NO:574 HELSNEERNLLSVAYKNVVG
SEQ ID NO:575 WRVISSIEQKTERNEKKQQM
SEQ ID NO:576 IEAELQDICNDVLELLDKYL
SEQ ID NO:577 GLALNFSVFYYEILNSPEKA
SEQ ID NO:578
LKMKG DYFRYLSEVASGDNKQTTVSNSQQAYQEAFEISKEMQPTHPIRL
SEQ ID NO:579
CSLAKTAFDEAIAELDTLNEESYKDSTLIMQLLRDNLTLWTSENQGDG

14-3-3z

SEQ ID NO:580 MDKNELVQKAKLAEQAERYD
SEQ ID NO:581 DMAACMKSVTEQGAELSNEE
SEQ ID NO:582 RNLLSVAYKNVVGARRSSWR
SEQ ID NO:583 IEQKTEGAEEKQQMAREYRE
SEQ ID NO:584 CNDVLSLLEKFLIPNASQAE
SEQ ID NO:585
MKG DYRYLA EVAAGDDKKGIVDQSQQAYQEAFEISKEMQPTHPIRLGL
SEQ ID NO:586
SPEKACSLAKTAFDEAIAELDTLSEESYKDSTLIMQLLRDNLTLWTSDTQ

FAK2

SEQ ID NO:587 PFFWLENKDVIGVLEKGDRL
SEQ ID NO:588 PKPDLCPVLYTLMTRCWDY
SEQ ID NO:589 CSLSDVYQMEKDIAMEQERN
SEQ ID NO:590 RPPPQTNLLAPKLQFQVPEG
SEQ ID NO:591 QMVEDYQWLRQEEKSLDPMV
SEQ ID NO:592
PEKEVGYLEFTGPPQKPPRLGAQSIQPTANLDRDLDVYLNVMELVRAVL
SEQ ID NO:593
PEGYVVVVKNVGLTLRKLIGSVDDLLPSLPSSSRTEIEGTQKLLNKDLAE

EPS8

SEQ ID NO:594 LFTPLNMVVQATGGPELASS
SEQ ID NO:595 MGATMEQDLYQLAESVANVA

SEQ ID NO:596 NIYTRGSHLDQGEAAVAFKP
SEQ ID NO:597 EILDDRKQWWKVRNASGDSG
SEQ ID NO:598 PYHTTIQKQRMEYGPRPADT
SEQ ID NO:599
SSDSGGSIVRDSQRHKQLPVDRRKSQMEEVQDELIHRLTIGRSAAQKKFH
SEQ ID NO:62 600
ITYDSTPEDVKTWLQSKGFNPVTVNSLGVLNGAQLFSLNKDELRTVCPEG

GASP

SEQ ID NO:601 LLMEKIRDPFIHEISKIAMG
SEQ ID NO:602 MRSASQFTRDFIRD SGVVSL
SEQ ID NO:603 IETLLNYPSSRVRTSFLENM
SEQ ID NO:604 IRMAPYPNLNIIQTYICKV
SEQ ID NO:605 CEETLAYSVDSPEQLSGIRM
SEQ ID NO:606
LTTTTDYHTLVANYMSGFLSLLATGNAKTRFHVLKMLLNLSENLFMTKEL
SEQ ID NO:607
FIGLFNREETNDNIQIVLAI FENIGNNIKKETVFSDDDFNIEPLISAFHK

Of SNCA(140) Interactors:

CTNND2

SEQ ID NO:608 SRLAKSYSTSSPINIVVSSA
SEQ ID NO:609 YSKHSQELYATATLQRP GSL
SEQ ID NO:610 RSLSQSQGVPLPPAHTGTYR
SEQ ID NO:611 SPYSKSGPALPPEGTLARSP
SEQ ID NO:612 LRNLVYGKANDDNKIALKNC
SEQ ID NO:613
NLSSCDALKMPIIQDALAVLTNAVIIPHSGWENSPLODDRKIQLHSSQVL
SEQ ID NO:614
VSSPGEEARRRMRECDGLTDALLYVIQSALGSSEIDSKTVENCVCILRNL

Of ERAB Interactors:

CTNND2

SEQ ID NO:615 PINIVVSSAGLSPIRVTSPP
SEQ ID NO:616 VHASEQYSKHSQELYATATL
SEQ ID NO:617 SPGVDSVPLQRTGSQHGPQN
SEQ ID NO:618 AAGPASNYADPYRQLQYCPS
SEQ ID NO:619 IQMLQHQPFSVQSNAAYLQ
SEQ ID NO:620
SSCDALKMPIIQDALAVLTNAVIIPHSGWENSPLODDRKIQLHSSQVLRLN
SEQ ID NO:621
NVSSPGEEARRRMRECDGLTDALLYVIQSALGSSEIDSKTVENCVCILRN

Of Bcl2-alpha Interactors:

CTNND2

SEQ ID NO:622 NVSSPGEEARRRMRECDGLT
SEQ ID NO:623 QGQHMGTDDEL DGLLCGEANG
SEQ ID NO:624 LWHPSIVKPYLTLLSECSNP
SEQ ID NO:625 LRIDNDRVACAVATALRNMA
SEQ ID NO:626 TAVCCTLHEVITKNMENAKA
SEQ ID NO:627
ISLKERKTDYECTGSNATYHGAKGEHTSRKDAMTAQNTGISTLYRNSYGA
SEQ ID NO:628
SAQPVPQEPSRKDYETYQPFQNSTRYNDESFEDQVHHRPPASEYTMHLG

Of AXIN Interactors:

cit-synt

SEQ ID NO:629 MALLTAAARLLGTKNASCLV
SEQ ID NO:630 LAARHASASSTNLKDILADL
SEQ ID NO:631 IPKEQARIKTFRQQHGKTVV
SEQ ID NO:632 GQITVDMMYGGMRGMKGLVY
SEQ ID NO:633 ETSVLDPDEGIRFRGFSIPE
SEQ ID NO:634
GMKGLVYETSVLDPDEGIRFRGFSIPECQKLLPKAKGGEEPLPEGLFWLL
SEQ ID NO:635
MALLTAAARLLGTKNASCLVLAARHASASSTNLKDILADLIPKEQARIKT

ALDOC

SEQ ID NO:636 LAAVYKALSDHHVYLEGTLL
SEQ ID NO:637 KPNMVTPGHACPIKYTPEEI
SEQ ID NO:638 AMATVTALRRTVPPAVPGVT
SEQ ID NO:639 FLSGGQSEEEASFNLNAINR
SEQ ID NO:640 CPLPRPWALTFSYGRALQAS
SEQ ID NO:641
ALNAWRGQRDNAGAATEEFIKRAEVNGLAAQGKYEGSGEDGGAAAQSLYI
SEQ ID NO:642
IKYTPEEIAMATVTALRRTVPPAVPGVTFLSGGQSEEEASFNLNAINRCP

CKB

SEQ ID NO:643 VDNPGHPYIMTVGCVAGDEE
SEQ ID NO:644 LDPNYVLSSRVRTGRSIRGF
SEQ ID NO:645 EAEQQQLIDDHFLFDKPVSP
SEQ ID NO:646 EDRHGGYKPSDEHKTDLNP
SEQ ID NO:647 ARGIVHNDNKTFVLVWVNEED
SEQ ID NO:648
TRFCTGLTQIETLFSKDYEFMWNPHLGYILTCPSNLGTGLRAGVHIKLP

SEQ ID NO:649
KHEKFSEVLKRLRLQKRGTTGGVDTAAVGGVFDVSNADRLGFSEVELVQMV

NRGN

SEQ ID NO:650 MDCCTENACSKPDDDDILDIP
SEQ ID NO:651 LDDPGANAAAAKIQASFRGH
SEQ ID NO:652 MARKKIKSGERGRKGPGPGG
SEQ ID NO:653
AKIQASFRGHMARKKIKSGERGRKGPGPGGMARKKIKSGERGRKGPGPGG

RAB3A

SEQ ID NO:654 MASATDSRYGQKESSDQNF
SEQ ID NO:655 YMFKILIIGNSSVGKTSFLF
SEQ ID NO:656 RYADDSFTPAFVSTVGIDFK
SEQ ID NO:657 VKTIYRNDKRIKLQIWDTAG
SEQ ID NO:658 QERYRTITTAYYRGAMGFIL
SEQ ID NO:659
VKTIYRNDKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITNEESF
SEQ ID NO:660
TDSRYGQKESSDQNFDMFKILIIGNSSVGKTSFLFRYADDSFTPAFVST

PRDX3

SEQ ID NO: MAAAVGRLLRASVARHVS
SEQ ID NO:661 HAPAVTQHAPYFKGTAVVNG
SEQ ID NO:662 EFHDVNCEVVAVSVDHFSH
SEQ ID NO:663 LALRGLFIIDPNGVIKHLV
SEQ ID NO:664 SPTIKPSPAASKEYFQKVNQ
SEQ ID NO:665
RASVARHVS
SEQ ID NO:666
EVVAVSVDSHFSHLAWINTPRKNGGLGHMNIALLSDLTKQISR
DYGVLL

SMN1

SEQ ID NO:667 MAMSSGGSGGGVPEQEDSVL
SEQ ID NO:668 KPKTTPKRKPAKKNKSQKKN
SEQ ID NO:669 ETCVVVYTGYNREEQNLSD
SEQ ID NO:670 DNIKPKSAPWNSFLPPPPM
SEQ ID NO:671 PIIPPPPPICPDSLDDADAL
SEQ ID NO:672
YGNREEQNLSDLLSPICEVANNIEQNAQENENESQVSTDESENSRSPGNK
SEQ ID NO:673
KPKTTPKRKPAKKNKSQKKN
TAA
SLQQWKVGDKCSAIWSE
DGC
IYPATIA

SFRS9

SEQ ID NO:674 GETSYIRVYPERSTSYGYSR
SEQ ID NO:675 SRSGSRGRDSPYQSRGSPHY
SEQ ID NO:676 RDS
PYQSRGSPHYFSPFRPY

Of TFCP2 Interactors:

APP695

SEQ ID NO:677 MLPGLALLLLAAWTARALEV
SEQ ID NO:678 TCIDTKEGILQYCQEVYPEL
SEQ ID NO:679 EFVSDALLVPDKCKFLHQER
SEQ ID NO:680 GVEFVCCPLAEESDNVDSAD
SEQ ID NO:681 NVDSADAEEDSDVWWGGAD
SEQ ID NO:682
QYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVG
SEQ ID NO:683
PDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKF

4F5S

SEQ ID NO:684 MARGNQRELARQKNMKKTQE
SEQ ID NO:685 ISKGKRKEDSLTASQRKQRD
SEQ ID NO:686 SEIMQEKQKAANEKKSMQTR
SEQ ID NO:687
MARGNQRELARQKNMKKTQEISKGKRKEDSLTASQRKQRDSEIMQEKQKA
SEQ ID NO:688
KNMKKTQEISKGKRKEDSLTASQRKQRDSEIMQEKQKAANEKKSMQTREK

PN7740 Peptide Inhibitors

SEQ ID NO:689
pqknvvthrlhl^{nr}fsvs^gtattysqssastyvptvcngrevldsttssl

SEQ ID NO:690
qknvvthrlhl^{nr}fsvs^gtattysqssastyvptvcngre

SEQ ID NO:691
Knvvthrlhl^{nr}fsvs^gtattysqssastyvptvc

SEQ ID NO:692
nvvtthrlhl^{nr}fsvs^gtattysqssastyv

SEQ ID NO:693
nvvtthrlhl^{nr}fsvs^gtattysqss

SEQ ID NO:694
thrlhl^{nr}fsvs^gtattysq

SEQ ID NO:695
hrlhl^{nr}fsvs^gtattys